
Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Tue May 15 12:31:12 EDT 2007

Validated By CRFValidator v 1.0.2

Application No: 10571667 Version No: 1.1

Input Set:

Output Set:

Started: 2007-05-15 12:30:57.314 **Finished:** 2007-05-15 12:30:58.489

Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 175 ms

Total Warnings: 10
Total Errors: 0

No. of SeqIDs Defined: 20

Actual SeqID Count: 20

Erro	or code	Error Descript	ion								
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(11)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(12)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(13)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(14)
M	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(15)
M	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(16)
M	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(17)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(18)
M	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(19)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(20)

```
<110> DE VRIES, Erik
GAFFAR, Fasilla Razzia
YATSUDA, Ana Patricia
SCHAAP, Theodorus Cornelis
<120> Piroplasmid vaccine
<130> I-2003.010 US
<140> 10/571,667
<141> 2006-03-14
<150> PCT/EP2004/052169
<151> 2004-09-14
<150> EP 03020898.7
<151> 2003-09-14
<160> 20
<170> PatentIn version 3.3
<210> 1
<211> 1818
<212> DNA
<213> Babesia bovis
<220>
<221> CDS
<222> (1)..(1818)
<400> 1
atg cag tta cat aac aaa atg cag tca act tct ctc aaa tat aac tac
                                                                      48
Met Gln Leu His Asn Lys Met Gln Ser Thr Ser Leu Lys Tyr Asn Tyr
               5
                                   10
aag cgc atg ctt tgt atg gct ctt gta cca gtt atc tta tcg tca ttt
Lys Arg Met Leu Cys Met Ala Leu Val Pro Val Ile Leu Ser Ser Phe
            20
                                25
ttt geg gaa gat get tta get tee aac tee aeg ett tte get tte eac
                                                                     144
Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His
        35
                            40
                                                45
aag gaa cca aac aat cgt agg ctt acc aaa agg tct tca aga gga cag
                                                                     192
Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln
    50
ttg ctc aac tca agg agg ggt tcg gat gat gcg tcc gaa tct tcc gat
                                                                     240
Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp
                    70
                                        75
```

aga tac cca ggt agg tcg ggt ggc tct aag aat tcg agc caa tcc ccc

288

Arg	Tyr	Pro	Gly	Arg 85	Ser	Gly	Gly	Ser	Lys 90	Asn	Ser	Ser	Gln	Ser 95	Pro	
		_		_	caa Gln	_		-			_					336
			-	-	ctt Leu				-		-				_	384
	_	_		_	ggt Gly	_	_		-	_					_	432
				-	gac Asp 150			-					-	-		480
_		_		_	gca Ala					-		-				528
				_	aca Thr	-					-			-		576
			_	_	gcg Ala		_	_	_	_				_		624
	-	-			tgc Cys		-		-	-					_	672
	-		_		aaa Lys 230						_		-	_	_	720
					ata Ile											768
			_	-	aac Asn	-		_		-	_			_		816
_		_	_		cct Pro		_	_	-		_	-				864
					gtt Val	-		-		-	_		_		-	912
	_	_		_	gcc Ala										_	960

305 310 315 320

																1000
_	gcc Ala		_		-			-		-		-		-	=	1008
				325					330					335	11010	
tgt	gca	gcc	att	tta	ttc	gat	aac	tct	gca	act	gac	ttg	aat	atc	gaa	1056
Cys	Ala	Ala		Leu	Phe	Asp	Asn		Ala	Thr	Asp	Leu		Ile	Glu	
			340					345					350			
act	gtt	220	c a a	cat	+++	aat	c a a	c++	222	c a a	+ + a	200	cat	aaa	ctt	1104
-	Val		-	-			-			-	-		-			1104
		355		1-			360		-1-			365	1-	1		
aaa	aga	ttg	aac	atg	tcg	aag	gtt	gca	aac	gct	att	ttt	tct	CCC	ctc	1152
Lys	Arg	Leu	Asn	Met	Ser	_	Val	Ala	Asn	Ala		Phe	Ser	Pro	Leu	
	370					375					380					
tcc	aat	at t	aca	aat	200	art	cas	att	tca	cat	aat	ata	aat	ato	aac	1200
	Asn	_	_			_	_			_				_		1200
385				1	390		5			395	1		1		400	
tgg	gct	aca	tac	gat	aaa	gat	tct	ggt	atg	tgt	gct	ctc	att	aac	gaa	1248
Trp	Ala	Thr	Tyr	Asp	Lys	Asp	Ser	Gly	Met	Cys	Ala	Leu	Ile	Asn	Glu	
				405					410					415		
202	cct	2.26	+ ~ ~	++~	2+0	++~	226	aaa	~~~	200	2++	aat	ata	2.00	aat	1296
	Pro		-	_		_				_		-		_	-	1230
			420					425	1				430			
ata	ggt	tca	cct	ctc	gag	tat	gac	gct	gtt	aac	tat	cct	tgc	cac	atc	1344
Ile	Gly		Pro	Leu	Glu	Tyr	Asp	Ala	Val	Asn	Tyr		CAa	His	Ile	
		435					440					445				
C a C	acc	aat	aat	tac	at t	nen	cca	cat	aca	220	aat	acc	aac	222	tac	1392
_	Thr				_			_	-	_						1372
	450		1	- 4 -		455		9			460				-1-	
ctt	gat	gtt	cct	ttc	gag	gtc	aca	act	gct	ttg	agc	atg	aag	aca	cta	1440
	Asp	Val	Pro	Phe		Val	Thr	Thr	Ala		Ser	Met	Lys	Thr		
465					470					475					480	
aaa	tgc	gat	acc	tat	att	cac	acc	aad	tac	t ct	gac	agt	tat	aat	acc	1488
	Cys	-	-		-			-			-	-	-			1100
-	_	-		485				_	490		-		_	495		
tat	ttc	ctt	tgc	tca	gac	gtc	aaa	cct	aac	tgg	ttc	att	agg	ttc	tta	1536
Tyr	Phe	Leu	_	Ser	Asp	Val	Lys		Asn	Trp	Phe	Ile	_	Phe	Leu	
			500					505					510			
cac	atg	atc	aaa	ata	tac	aac	aca	aan	cat	atc	ata	ata	tta	ata	tac	1584
	Met							_	-		-				_	
		515	_		-		520	-	_			525			-	
_	acc			_		_								_		1632
Cys	Thr	Thr	Thr	Ala	Ile	Val	Leu	Thr	Ile	Trp	Ile	Trp	Lys	Arg	Phe	
	530					535					540					

		_	agt ttc gac aa Ser Phe Asp Ly 555	
-	_	_	gcc gac aac ga Ala Asp Asn Gl	
	Ser Ser Ala		gga gag gct gt Gly Glu Ala Va 59	l Gln Arg
cca agt gat gto Pro Ser Asp Val 595	_		aaa atc aac ta Lys Ile Asn 605	a 1818
<210> 2 <211> 605 <212> PRT <213> Babesia	bovis			
Met Gln Leu His	s Asn Lys Met 5	Gln Ser Thr	Ser Leu Lys Ty	r Asn Tyr 15
Lys Arg Met Leu 20	ı Cys Met Ala	. Leu Val Pro 25	Val Ile Leu Se 30	r Ser Phe
Phe Ala Glu Asp 35	o Ala Leu Ala	. Ser Asn Ser 40	Thr Leu Phe Al	a Phe His
Lys Glu Pro Asr 50	n Asn Arg Arg 55	Leu Thr Lys	Arg Ser Ser Ar	g Gly Gln
Leu Leu Asn Sei 65	Arg Arg Gly 70	Ser Asp Asp	Ala Ser Glu Se 75	r Ser Asp 80
Arg Tyr Pro Gly	Arg Ser Gly 85	Gly Ser Lys 90	Asn Ser Ser Gl	n Ser Pro 95
Trp Ile Lys Tyn	_	Phe Asp Ile 105	Pro Arg Asn Hi 11	_
Gly Ile Tyr Val	Asp Leu Gly	Gly Tyr Glu 120	Ser Val Gly Se	r Lys Ser

Tyr	Arg 130	Met	Pro	Val	Gly	Lys 135	Суз	Pro	Val	Val	Gly 140	Lys	Ile	Ile	Asp
Leu 145	Gly	Asn	Gly	Ala	Asp 150	Phe	Leu	Asp	Pro	Ile 155	Ser	Ser	Asp	Asp	Pro 160
Ser	Tyr	Arg	Gly	Leu 165	Ala	Phe	Pro	Glu	Thr 170	Ala	Val	Asp	Ser	Asn 175	Ile
Pro	Thr	Gln	Pro 180	Lys	Thr	Arg	Gly	Ser 185	Ser	Ser	Ala	Ser	Ala 190	Ala	Lys
Leu	Ser	Pro 195	Val	Ser	Ala	Lys	Asp 200	Leu	Arg	Arg	Trp	Gly 205	Tyr	Glu	Gly
Asn	Asp 210	Val	Ala	Asn	Cys	Ser 215	Glu	Tyr	Ala	Ser	Asn 220	Leu	Ile	Pro	Ala
Ser 225	Asp	Arg	Ser	Thr	Lys 230	Tyr	Arg	Tyr	Pro	Phe 235	Val	Phe	Asp	Ser	Asp 240
Asn	Gln	Met	Суз	Tyr 245	Ile	Leu	Tyr	Ser	Ala 250	Ile	Gln	Tyr	Asn	Gln 255	Gly
Asn	Arg	Tyr	Cys 260	Asp	Asn	Asp	Gly	Ser 265	Ser	Glu	Asp	Gly	Thr 270	Ser	Ser
		275					280					285	His		
_	290					295					300		Cys		
305					310					315			Gly		320
				325					330				Thr	335	
Cys	Ala	Ala	11e 340	Leu	Phe	Asp	Asn	Ser 345	Ala	Thr	Asp	Leu	Asn 350	Ile	Glu

Ala Val Asn Glu Asp Phe Asn Glu Leu Lys Glu Leu Thr Asp Gly Leu

355 360 365

Lys Arg Leu Asn Met Ser Lys Val Ala Asn Ala Ile Phe Ser Pro Leu 370 375 380 Ser Asn Val Ala Gly Thr Ser Arg Ile Ser Arg Gly Val Gly Met Asn 385 390 395 Trp Ala Thr Tyr Asp Lys Asp Ser Gly Met Cys Ala Leu Ile Asn Glu 405 410 415 Thr Pro Asn Cys Leu Ile Leu Asn Ala Gly Ser Ile Ala Leu Thr Ala 420 425 Ile Gly Ser Pro Leu Glu Tyr Asp Ala Val Asn Tyr Pro Cys His Ile 435 440 445 Asp Thr Asn Gly Tyr Val Glu Pro Arg Ala Lys Asn Thr Asn Lys Tyr 450 455 460 Leu Asp Val Pro Phe Glu Val Thr Thr Ala Leu Ser Met Lys Thr Leu 465 470 475 480 Lys Cys Asp Ala Tyr Val His Thr Lys Tyr Ser Asp Ser Cys Gly Thr 485 490 495 Tyr Phe Leu Cys Ser Asp Val Lys Pro Asn Trp Phe Ile Arg Phe Leu 500 505 510 His Met Ile Gly Leu Tyr Asn Thr Lys Arg Ile Val Ile Phe Val Cys 515 520 525 Cys Thr Thr Thr Ala Ile Val Leu Thr Ile Trp Ile Trp Lys Arg Phe 530 535 540 Ile Lys Ala Lys Lys Glu Pro Ala Pro Pro Ser Phe Asp Lys Tyr Leu 545 550 555 560 Ser Asn Tyr Asp Tyr Asp Thr Thr Leu Asp Ala Asp Asn Glu Thr Glu 570 575 565

Gln Arg Leu Asp Ser Ser Ala Tyr Ser Trp Gly Glu Ala Val Gln Arg

585

590

580

Pro Ser Asp Val Thr Pro Val Lys Leu Ser Lys Ile Asn 595 600 605

<213 <213	<210> 3 <211> 2349 <212> DNA <213> Theileria annulata																
<223	<220> <221> CDS <222> (1)(2349)																
< 400)> 3	3															
atg	aaa	aaa	ata	gga	ctt	aaa	att	agg	gca	caa	aag	gat	aaa	tta	aat	48	
Met 1	Lys	Lys	Ile	Gly 5	Leu	Lys	Ile	Arg	Ala 10	Gln	Lys	Asp	Lys	Leu 15	Asn		
cct	gtg	tta	gga	agc	aac	tct	gac	cct	tca	gaa	gag	tat	gat	tca	ttc	96	
	Val			-			-		_	-			-				
a a a	caa	a a t	a++	++a	act	a a t	C 2 2	aa a	200	C 2 2	at a	C a C	222	t at	cat	144	
_	Gln		-													111	
cac	tac	att	aca	cac	cad	aaa	aaa	acc	adc	caa	cac	atc	gac	gat	tta	192	
	Tyr 50								-				-	-		172	
aat	ttt	tat	aat	qqa	aaa	ttt	aat	caa	aaq	agc	aga	att	aat	cca	aaa	240	
	Phe								_	_	_						
65					70					75					80		
aag	gta	gta	aat	aac	agt	agg	aat	ctg	gta	gaa	ggt	gaa	aca	cta	tct	288	
Lys	Val	Val	Asn	Asn 85	Ser	Arg	Asn	Leu	Val 90	Glu	Gly	Glu	Thr	Leu 95	Ser		
aag	gat	gac	aat	aaa	aca	aaa	tct	aaa	ata	aag	tca	aaa	aca	gca	tca	336	
Lys	Asp	Asp	Asn 100	Lys	Thr	Lys	Ser	Lys 105	Ile	Lys	Ser	Lys	Thr 110	Ala	Ser		
att	tta	cct	aga	ctt	tta	aaa	tct	tta	tca	ttt	tta	gct	gtt	tta	ggg	384	
	Leu		-										-		-		
		115					120					125					
tca	att	aat	tca	ttt	tca	tta	gca	tta	gag	gaa	cct	ttt	act	caa	cac	432	
Ser	11e 130	Asn	Ser	Phe	Ser	Leu 135	Ala	Leu	Glu	Glu	Pro 140	Phe	Thr	Gln	His		
act	tct	aac	cga	acg	ccc	ttt	gaa	gta	tca	tta	att	caa	agc	aac	agc	480	
Thr	Ser	Asn	Arg	Thr	Pro	Phe	Glu	Val	Ser	Leu	Ile	Gln	Ser	Asn	Ser		
145					150					155					160		

agt	tta	tcg	cct	att	cat	aat	tct	tca	act	caa	aat	tca	agt	cat	cac	528
Ser	Leu	Ser	Pro	Ile	His	Asn	Ser	Ser	Thr	Gln	Asn	Ser	Ser	His	His	
				165					170					175		
aac	ggt	ttt	agt	ggt	agt	acc	gtt	aat	aat	acc	tca	tta	ata	gag	aca	576
Asn	Gly	Phe	Ser	Gly	Ser	Thr	Val	Asn	Asn	Thr	Ser	Leu	Ile	Glu	Thr	
			180					185					190			
agg	aat	aac	gta	tta	aac	aga	aca	cta	ggt	aga	ttc	gga	tca	ttt	ttg	624
Arq	Asn	Asn	Val	Leu	Asn	Arq	Thr	Leu	Glv	Arq	Phe	Glv	Ser	Phe	Leu	
_		195				_	200		_	_		205				
caa	tca	gga	ttg	ata	agc	agt	aga	gca	gac	aaa	aag	aag	cgg	tct	ggt	672
Gln	Ser	Gly	Leu	Ile	Ser	Ser	Arg	Ala	Asp	Lys	Lys	Lys	Arg	Ser	Gly	
	210					215			_		220		_		_	
atg	aat	aga	aga	ggc	cct	aag	ddd	aag	aaa	ggg	aag	gga	gga	gaa	gac	720
	Asn															
225		,	,	_	230	_	_	_	_	235	_	_	_		240	
maa.	gaa	220	aaa	220	nss	t aa	acc	cat	t t c	ata	aca	220	+++	cat	atc	768
_	-	_			aag	cgg	acc	gat		acg	gca	aag		gat	acc	, 50
GIU	Glu	туз	Arg	A												